SEQUENCE LISTING

<110> Medical Research Council

<120>   Obesity Gene

<130>   18396/1140

<140>   09/484,629
<141>   2000-01-18

<150>   GB 9910522.3
<151>   1999-05-06

<160>   46

<170>   PatentIn version 3.0

<210>   1
<211>   924
<212>   DNA
<213>   Rattus sp.

<220>
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<222>   (5)..(607)

<400>   1
tgtc atg ttg cgg gct ttg aac cgc ctg gcc gcg cgg ccc ggg ggc cag   49
     Met Leu Arg Ala Leu Asn Arg Leu Ala Ala Arg Pro Gly Gly Gln
      1   5   10   15

ccc cca acc ctg ctc ctt ctg ccc gtg cgc ggc cgc aag acc cgc cac   97
Pro Pro Thr Leu Leu Leu Leu Pro Val Arg Gly Arg Lys Thr Arg His
                 20   25   30

gat ccg cct gcc aag tcc aag gtc ggg cgc gtg aaa atg cct cct gca   145
Asp Pro Pro Ala Lys Ser Lys Val Gly Arg Val Lys Met Pro Pro Ala
                 35   40   45

gtg gac cct gcg gaa ttg ttc gtg ttg acc gag cgc tac cga cag tac   193
Val Asp Pro Ala Glu Leu Phe Val Leu Thr Glu Arg Tyr Arg Gln Tyr
             50   55   60

cgg gag acg gtg cgc gct ctc agg cga gag ttc aca ttg gag gtg cga   241
Arg Glu Thr Val Arg Ala Leu Arg Arg Glu Phe Thr Leu Glu Val Arg
         65   70   75

ggg aaa ttg cac gag gcc cga gcc ggg gtt ctg gct gag cgc aag gcg   289
Gly Lys Leu His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala
80   85   90   95

caa gag gcc atc aga gag cac cag gag ctg atg gcc tgg aac cgg gag   337
Gln Glu Ala Ile Arg Glu His Gln Glu Leu Met Ala Trp Asn Arg Glu
                100   105   110

gag aac cgg aga ctg cag gaa cta cgg ata gct agg ttg cag ctc gaa   385
Glu Asn Arg Arg Leu Gln Glu Leu Arg Ile Ala Arg Leu Gln Leu Glu
                115   120   125

gca cag gcc cag gag ctg cgg cag gct gag gtc cag gcc cag agg gcc   433

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Ala Gln Ala Gln Glu Leu Arg Gln Ala Glu Val Gln Ala Gln Arg Ala
        130                 135                 140

cag gag gag cag gct tgg gtg caa ctg aaa gaa caa gaa gtt ctc aaa    481
Gln Glu Glu Gln Ala Trp Val Gln Leu Lys Glu Gln Glu Val Leu Lys
        145                 150                 155

ctg cag gag gag gcc aaa aac ttc atc act cgg gag aac ctg gag gca    529
Leu Gln Glu Glu Ala Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala
160                 165                 170                 175

cgg ata gaa gag gcc ttg gac tct ccg aag agt tat aac tgg gcg gtc    577
Arg Ile Glu Glu Ala Leu Asp Ser Pro Lys Ser Tyr Asn Trp Ala Val
                180                 185                 190

acc aaa gaa ggg cag gtg gtc agg aac tga gaacagaggc ctctcaggcc      627
Thr Lys Glu Gly Gln Val Val Arg Asn
                    195             200

caaataagga cagtgcttgc ctagggactg gatattgggg tagaaattgg tgcatcccag   687

gagggtggca cagccttgtc cagagcagcc cccattcatt ctagatttgg caccaggtat   747

agtacctgtt ctgacaccac atacaaactc cggacagcat taaactctgg gaagttccta   807

tcacacagaa gatcagactg gactgtcccc tctagaagcc aagagctgtc tcctgagttt   867

cttggaatag tgtgagccca atgtttcctg cttttataaa taaactattg gaaagca      924


<210>   2
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<212>   PRT
<213>   Rattus sp.

<400>   2

Met Leu Arg Ala Leu Asn Arg Leu Ala Ala Arg Pro Gly Gly Gln Pro
1               5                   10                  15


Pro Thr Leu Leu Leu Leu Pro Val Arg Gly Arg Lys Thr Arg His Asp
                20                  25                  30


Pro Pro Ala Lys Ser Lys Val Gly Arg Val Lys Met Pro Pro Ala Val
            35                  40                  45


Asp Pro Ala Glu Leu Phe Val Leu Thr Glu Arg Tyr Arg Gln Tyr Arg
        50                  55                  60


Glu Thr Val Arg Ala Leu Arg Arg Glu Phe Thr Leu Glu Val Arg Gly
65                  70                  75                  80


Lys Leu His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Gln
                85                  90                  95
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Glu Ala Ile Arg Glu His Gln Glu Leu Met Ala Trp Asn Arg Glu Glu
            100             105             110

Asn Arg Arg Leu Gln Glu Leu Arg Ile Ala Arg Leu Gln Leu Glu Ala
            115             120             125

Gln Ala Gln Glu Leu Arg Gln Ala Glu Val Gln Ala Gln Arg Ala Gln
    130             135             140

Glu Glu Gln Ala Trp Val Gln Leu Lys Glu Gln Glu Val Leu Lys Leu
145             150             155             160

Gln Glu Glu Ala Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala Arg
                165             170             175

Ile Glu Glu Ala Leu Asp Ser Pro Lys Ser Tyr Asn Trp Ala Val Thr
                180             185             190

Lys Glu Gly Gln Val Val Arg Asn
            195             200


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<213>   Rattus sp.

<220>
<221>   CDS
<222>   (1)..(996)

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Met Leu Arg Ala Leu Ser Arg Leu Gly Ala Gly Thr Pro Cys Arg Pro
1               5                   10                  15

cgg gcc cct ctg gtg ctg cca gcg cgc ggc cgc aag acc cgc cac gac      96
Arg Ala Pro Leu Val Leu Pro Ala Arg Gly Arg Lys Thr Arg His Asp
                20                  25                  30

ccg ctg gcc aaa tcc aag atc gag cga gtg aac atg ccg ccc gcg gtg      144
Pro Leu Ala Lys Ser Lys Ile Glu Arg Val Asn Met Pro Pro Ala Val
            35                  40                  45

gac cct gcg gag ttc ttc gtg ctg atg gag cgt tac cag cac tac cgc      192
Asp Pro Ala Glu Phe Phe Val Leu Met Glu Arg Tyr Gln His Tyr Arg
        50                  55                  60

cag acc gtg cgc gcc ctc agg atg gag ttc gtg tcc gag gtg cag agg      240
Gln Thr Val Arg Ala Leu Arg Met Glu Phe Val Ser Glu Val Gln Arg
65                  70                  75                  80

aag gtg cac gag gcc cga gcc ggg gtt ctg gcg gag cgc aag gcc ctg      288
Lys Val His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Leu
                85                  90                  95
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aag gac gcc gcc gag cac cgc gag ctg atg gcc tgg aac cag gcg gag        336
Lys Asp Ala Ala Glu His Arg Glu Leu Met Ala Trp Asn Gln Ala Glu
            100             105             110

aac cgg cgg ctg cac gag ctg cgg ata gcg agg ctg cgg cag gag gag        384
Asn Arg Arg Leu His Glu Leu Arg Ile Ala Arg Leu Arg Gln Glu Glu
            115             120             125

cgg gag cag gag cag cgg cag gcg ttg gag cag gcc cgc aag gcc gaa        432
Arg Glu Gln Glu Gln Arg Gln Ala Leu Glu Gln Ala Arg Lys Ala Glu
            130             135             140

gag gtg cag gcc tgg gcg cag cgc aag gag cgg gaa gtg ctg cag ctg        480
Glu Val Gln Ala Trp Ala Gln Arg Lys Glu Arg Glu Val Leu Gln Leu
145             150             155             160

cag gaa gag gtg aaa aac ttc atc acc cga gag aac ctg gag gca cgg        528
Gln Glu Glu Val Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala Arg
                165             170             175

gtg gaa gca gca ttg gac tcc cgg aag aac tac aac tgg gcc atc acc        576
Val Glu Ala Ala Leu Asp Ser Arg Lys Asn Tyr Asn Trp Ala Ile Thr
            180             185             190

aga gag ggg ctg gtg gtc agg cca caa cgc agg gac tcc tag ggg ccc        624
Arg Glu Gly Leu Val Val Arg Pro Gln Arg Arg Asp Ser     Gly Pro
            195             200             205

agt aag gac agt gcc cgc cag gga cca tgt atg tat cat ggc gga aga        672
Ser Lys Asp Ser Ala Arg Gln Gly Pro Cys Met Tyr His Gly Gly Arg
            210             215             220

gtt ggc cct gac ctg gaa taa agc agt tgg tgt tgc tta tga gga agg        720
Val Gly Pro Asp Leu Glu     Ser Ser Trp Cys Cys Leu     Gly Arg
            225             230             235

ttc agc ctt atc cag cac agc ctt cac gtt ttg ccc tct gct gtc acc        768
Phe Ser Leu Ile Gln His Ser Leu His Val Leu Pro Ser Ala Val Thr
            240             245             250

act tgg tca gaa act tcc aaa cgc agt gcc ctg ttc tgc cgg tgt gta        816
Thr Trp Ser Glu Thr Ser Lys Arg Ser Ala Leu Phe Cys Arg Cys Val
            255             260             265

aag cct cag cgc acc agg aga ccc tag agt ggt ttc cat ctc aca gag        864
Lys Pro Gln Arg Thr Arg Arg Pro     Ser Gly Phe His Leu Thr Glu
270             275             280

aat cag aca ggc cac agc ccc ctc agg cag cca ggt cat ctg agt atc        912
Asn Gln Thr Gly His Ser Pro Leu Arg Gln Pro Gly His Leu Ser Ile
285             290             295             300

att aag agt agt gat ggg aag att aca gtc tga ggg cca aac gtg cct        960
Ile Lys Ser Ser Asp Gly Lys Ile Thr Val     Gly Pro Asn Val Pro
                305             310             315

gct tcc tgt ttt tgt aaa taa agt ttt gtt gga aca ca                     998
Ala Ser Cys Phe Cys Lys     Ser Phe Val Gly Thr
                320             325
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<210> 4
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<212> PRT
<213> Rattus sp.

<400> 4

Met Leu Arg Ala Leu Ser Arg Leu Gly Ala Gly Thr Pro Cys Arg Pro
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Arg Ala Pro Leu Val Leu Pro Ala Arg Gly Arg Lys Thr Arg His Asp
                20   25   30

Pro Leu Ala Lys Ser Lys Ile Glu Arg Val Asn Met Pro Pro Ala Val
                35   40   45

Asp Pro Ala Glu Phe Phe Val Leu Met Glu Arg Tyr Gln His Tyr Arg
        50   55   60

Gln Thr Val Arg Ala Leu Arg Met Glu Phe Val Ser Glu Val Gln Arg
65   70   75   80

Lys Val His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Leu
                85   90   95

Lys Asp Ala Ala Glu His Arg Glu Leu Met Ala Trp Asn Gln Ala Glu
                100   105   110

Asn Arg Arg Leu His Glu Leu Arg Ile Ala Arg Leu Arg Gln Glu Glu
        115   120   125

Arg Glu Gln Glu Gln Arg Gln Ala Leu Glu Gln Ala Arg Lys Ala Glu
        130   135   140

Glu Val Gln Ala Trp Ala Gln Arg Lys Glu Arg Glu Val Leu Gln Leu
145   150   155   160

Gln Glu Glu Val Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala Arg
                165   170   175

Val Glu Ala Ala Leu Asp Ser Arg Lys Asn Tyr Asn Trp Ala Ile Thr
                180   185   190

Arg Glu Gly Leu Val Val Arg Pro Gln Arg Arg Asp Ser
        195   200   205

<210> 5

<211> 24
<212> PRT
<213> Rattus sp.

<400> 5

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1   5   10   15

Gly Arg Val Gly Pro Asp Leu Glu
            20

<210> 6
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<213> Rattus sp.

<400> 6

Ser Ser Trp Cys Cys Leu
1   5

<210> 7
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<212> PRT
<213> Rattus sp.

<400> 7

Gly Arg Phe Ser Leu Ile Gln His Ser Leu His Val Leu Pro Ser Ala
1   5   10   15

Val Thr Thr Trp Ser Glu Thr Ser Lys Arg Ser Ala Leu Phe Cys Arg
            20   25   30

Cys Val Lys Pro Gln Arg Thr Arg Arg Pro
            35   40

<210> 8
<211> 33
<212> PRT
<213> Rattus sp.

<400> 8

Ser Gly Phe His Leu Thr Glu Asn Gln Thr Gly His Ser Pro Leu Arg
1   5   10   15

Gln Pro Gly His Leu Ser Ile Ile Lys Ser Ser Asp Gly Lys Ile Thr
            20   25   30

Val

<210> 9
<211> 11
<212> PRT
<213> Rattus sp.

<400> 9

Gly Pro Asn Val Pro Ala Ser Cys Phe Cys Lys
1   5   10

<210> 10
<211> 5
<212> PRT
<213> Rattus sp.

<400> 10

Ser Phe Val Gly Thr
1   5

<210> 11
<211> 943
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(615)

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Cys His Val Ala Arg Ser Glu Pro Pro Gly Ala Ala Ala Gly Arg Pro
1   5   10   15

gcc ccc gac ccc gct gct cct gcc cgt gcg cgg ccg caa gac ccg cca   96
Ala Pro Asp Pro Ala Ala Pro Ala Arg Ala Arg Pro Gln Asp Pro Pro
                20   25   30

tga ccc gcc tgc caa atc caa ggt cgg acg ggt gca gac gcc tcc cgc   144
    Pro Ala Cys Gln Ile Gln Gly Arg Thr Gly Ala Asp Ala Ser Arg
        35   40   45

cgt gga ccc tgc gga att ctt cgt gtt gac cga gcg cta cgg aca gta   192
Arg Gly Pro Cys Gly Ile Leu Arg Val Asp Arg Ala Leu Arg Thr Val
        50   55   60

ccg gga gac cgt gcg cgc tct cag gct aga gtt cac gtt gga tgt gcg   240
Pro Gly Asp Arg Ala Arg Ser Gln Ala Arg Val His Val Gly Cys Ala
    65   70   75

aag gaa att gca cga ggc ccg agc cgg ggt tct ggc cga gcg caa ggc   288
Lys Glu Ile Ala Arg Gly Pro Ser Arg Gly Ser Gly Arg Ala Gln Gly
80   85   90   95

gca gca ggc cat cac gga gca ccg gga gct gat ggc ctg gaa ccg gga   336
Ala Ala Gly His His Gly Ala Pro Gly Ala Asp Gly Leu Glu Pro Gly
                100   105   110

```
cga gaa ccg gcg aat gca gga gct acg gat agc gag gtt gca gct gga      384
Arg Glu Pro Ala Asn Ala Gly Ala Thr Asp Ser Glu Val Ala Ala Gly
            115                 120                 125

agc aca ggc cca gga ggt gca gaa ggc tga ggc cca gcg cca gag ggc      432
Ser Thr Gly Pro Gly Gly Ala Glu Gly     Gly Pro Ala Pro Glu Gly
            130             135                     140

tca gga gga gca ggc ttg ggt gca act gaa aga gca aga agt gct caa      480
Ser Gly Gly Ala Gly Leu Gly Ala Thr Glu Arg Ala Arg Ser Ala Gln
            145             150             155

gct gca gga gga ggc aaa aaa ctt cat cac tcg gga gaa cct gga ggc      528
Ala Ala Gly Gly Gly Lys Lys Leu His His Ser Gly Glu Pro Gly Gly
        160             165             170

acg gat aga aga agc gtt gga ctc tcc gaa gag tta caa ctg ggc cgt      576
Thr Asp Arg Arg Ser Val Gly Leu Ser Glu Glu Leu Gln Leu Gly Arg
175                 180             185                 190

cac caa aga agg gca ggt ggt cag gaa ctg agc aca gag acttctgggg       625
His Gln Arg Arg Ala Gly Gly Gln Glu Leu Ser Thr Glu
                195                 200

gcccaaataa gcacagtgct tgcctagggt ctgtgtactg ggataggaat tggtacatcc    685

caggaggatg gctcagccgt ttccagagca acctcagtca ctccaggctc ggcactcacc    745

acctgactgg gaactcccag atgtccctgt tctggcacca cagtcaaact gagggcagca    805

ttaaactctg ggaagttcct atcgcacaga ggatcggact ggactgtgtc cctctagaag    865

ccaagcttgt cttgtaagtc tcttggagtc ctgtgagcca aatgtttcct gcttttataa    925

ataaagtatt ggagccca                                                  943


<210>   12
<211>   32
<212>   PRT
<213>   Homo sapiens

<400>   12

Cys His Val Ala Arg Ser Glu Pro Pro Gly Ala Ala Ala Gly Arg Pro
1                 5                 10                  15


Ala Pro Asp Pro Ala Ala Pro Ala Arg Ala Arg Pro Gln Asp Pro Pro
            20                  25                  30


<210>   13
<211>   104
<212>   PRT
<213>   Homo sapiens

<400>   13

Pro Ala Cys Gln Ile Gln Gly Arg Thr Gly Ala Asp Ala Ser Arg Arg
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                    1              5                      10                     15

Gly Pro Cys Gly Ile Leu Arg Val Asp Arg Ala Leu Arg Thr Val Pro
              20                25                30


Gly Asp Arg Ala Arg Ser Gln Ala Arg Val His Val Gly Cys Ala Lys
          35            40            45


Glu Ile Ala Arg Gly Pro Ser Arg Gly Ser Gly Arg Ala Gln Gly Ala
      50              55            60


Ala Gly His His Gly Ala Pro Gly Ala Asp Gly Leu Glu Pro Gly Arg
65              70            75                  80


Glu Pro Ala Asn Ala Gly Ala Thr Asp Ser Glu Val Ala Ala Gly Ser
              85            90                  95


Thr Gly Pro Gly Gly Ala Glu Gly
          100
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<210>   14
<211>   67
<212>   PRT
<213>   Homo sapiens

<400>   14

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Gly Pro Ala Pro Glu Gly Ser Gly Gly Ala Gly Leu Gly Ala Thr Glu
1               5                 10                  15


Arg Ala Arg Ser Ala Gln Ala Ala Gly Gly Gly Lys Lys Leu His His
              20            25                  30


Ser Gly Glu Pro Gly Gly Thr Asp Arg Arg Ser Val Gly Leu Ser Glu
          35              40            45


Glu Leu Gln Leu Gly Arg His Gln Arg Arg Ala Gly Gly Gln Glu Leu
          50              55            60


Ser Thr Glu
65
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<210>   15
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<212>   DNA
<213>   Homo sapiens

<220>
<221>   CDS

<222> (1)..(615)

<400> 15

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    1               5                       10

ata tag tga gac ctg tgc aag gaa gga tgg agt gca cgt tcc ctg atg    96
Ile         Asp Leu Cys Lys Glu Gly Trp Ser Ala Arg Ser Leu Met
            15              20              25

ttc aga gca acc ctg tgt cac tcc agg tag gtg aga tga gag gaa gag   144
Phe Arg Ala Thr Leu Cys His Ser Arg     Val Arg     Glu Glu Glu
        30              35                          40

ggt ggc ctt ggc ctg ggc ctc cta cgg gcc tgg aag ttg gga gaa gga   192
Gly Gly Leu Gly Leu Gly Leu Leu Arg Ala Trp Lys Leu Gly Glu Gly
            45              50              55

tgt aag cag act ctg ttc tct tct gag aaa tat cag gta ttg cag tca   240
Cys Lys Gln Thr Leu Phe Ser Ser Glu Lys Tyr Gln Val Leu Gln Ser
        60              65              70

gcc cag gct cct cag acc ctc cta agt gca gat tct ctg cag aat ctg   288
Ala Gln Ala Pro Gln Thr Leu Leu Ser Ala Asp Ser Leu Gln Asn Leu
    75              80              85

gtg ttg aca aca cta atg agt agg atg aga ctt cag ttc cct agc cct   336
Val Leu Thr Thr Leu Met Ser Arg Met Arg Leu Gln Phe Pro Ser Pro
90              95              100             105

cac cgt cag ctt ctg att acc aac aac tct ccc aga gga gag cca tct   384
His Arg Gln Leu Leu Ile Thr Asn Asn Ser Pro Arg Gly Glu Pro Ser
            110             115             120

acc ttt ggg aca gat gct ctc tgc cct gca ctg cct cct gtt tct ctt   432
Thr Phe Gly Thr Asp Ala Leu Cys Pro Ala Leu Pro Pro Val Ser Leu
            125             130             135

cat tgt aga gga aga tag tac ttt aaa agc ttc ata aat ggt ctc aag   480
His Cys Arg Gly Arg     Tyr Phe Lys Ser Phe Ile Asn Gly Leu Lys
        140             145             150

gtg gga aga ccc cgg ctc agg tga aag agg aca agc gtc acc tca cac   528
Val Gly Arg Pro Arg Leu Arg     Lys Arg Thr Ser Val Thr Ser His
        155             160             165

agg cca ccc agt aga aaa caa gtg atc act gat act gag aac tct ggc   576
Arg Pro Pro Ser Arg Lys Gln Val Ile Thr Asp Thr Glu Asn Ser Gly
        170             175             180

aat tgc aga gct gcc caa gac cac aac agg gca gtg caa tgcaggaaa    625
Asn Cys Arg Ala Ala Gln Asp His Asn Arg Ala Val Gln
    185             190             195

aggtttgttg ctcgattgca aacctaaagt ttaaagtgca tcaggagaac gcttactcaa   685

agaggaagtg taagcctaac ttaagtagct agaagctcag aatttcttgc atcagccctg   745

gaagggtaca caggccaccg gtgggccaga gaaccacacg ctttggggcg gtgtccaagc   805
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ttgtgaacaa gtaggcaaga gcgcctggtg ttgtagctgt cattggcggg caatacagcc    865
cagcgaactg tggtctccaa ggtgcccctc gaccctccca ctctacccga gactccaggg    925
acgcgatggg ccagacagca agagctccgc ctacgggggc ggggacagga gattcccgtg    985
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aaccataaat gagaatggag ctgttttat tgtgtaaggg agagtgacaa ggttgagaga   1525
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gaagatcaga ctggactgtc ccctctagaa gccaagagct gtctcctgag tttcttggaa   2185
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gcctcagaga atgcatctgc gtatgcttgc ctggcgctgg aattcggtgc acatggcttt    2785

gatgtgtacc ggggatcaga cacagatgtt tcatgagtgc agtgcatgcc tgttagtggt    2845

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<210>   16
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<212>   PRT
<213>   Homo sapiens

<400>   16

Pro Leu Trp Ile
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<210>   17
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<212>   PRT
<213>   Homo sapiens

<400>   17

Tyr Thr Cys Lys
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<210>   18
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<212>   PRT
<213>   Homo sapiens

<400>   18

Gln Thr Ile Arg Ala Ile
1   5

<210>   19
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<212>   PRT
<213>   Homo sapiens

<400>   19

Asp Leu Cys Lys Glu Gly Trp Ser Ala Arg Ser Leu Met Phe Arg Ala
1   5   10   15

Thr Leu Cys His Ser Arg
            20

<210>   20
<211>   104
<212>   PRT

<213> Homo sapiens

<400> 20

Glu Glu Glu Gly Gly Leu Gly Leu Gly Leu Leu Arg Ala Trp Lys Leu
1   5   10   15

Gly Glu Gly Cys Lys Gln Thr Leu Phe Ser Ser Glu Lys Tyr Gln Val
            20   25   30

Leu Gln Ser Ala Gln Ala Pro Gln Thr Leu Leu Ser Ala Asp Ser Leu
            35   40   45

Gln Asn Leu Val Leu Thr Thr Leu Met Ser Arg Met Arg Leu Gln Phe
        50   55   60

Pro Ser Pro His Arg Gln Leu Leu Ile Thr Asn Asn Ser Pro Arg Gly
65   70   75   80

Glu Pro Ser Thr Phe Gly Thr Asp Ala Leu Cys Pro Ala Leu Pro Pro
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Val Ser Leu His Cys Arg Gly Arg
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